IN THE CLAIMS

Please amend the Claims as follows.

Please cancel Claims 5, 7, 8, and 10.

Please substitute the amended Claims below for the correspondingly numbered pending claims. A marked-up version of the amended claims showing changes made is attached.

1. (amended) A method for detecting or quantifying a target nucleic acid in a sample comprising:

(a) preparing at least one primer specifically matched to a predetermined position of the target nucleic acid;

(b) annealing the at least one primer from (a) with the target nucleic acid to obtain a primer-nucleic acid duplex at the predetermined position of the target nucleic acid;

(c) mixing the primer-nucleic acid duplex from (b) with a non-terminator nucleotide mixture, wherein at least one of four required types of nucleotides for continuous extension during primer extension reactions is omitted from the non-terminator nucleotide mixture, and wherein at least one non-terminator nucleotide is labeled with a detectable marker;

(d) performing isometric primer extension by enzymatic or chemical reaction in an appropriate buffer to form isometric primer extension products, wherein the primer extension terminates at a target nucleic acid nucleotide complementary to the omitted non-terminator nucleotide of (c); and

(e) detecting or quantifying the amount of labeling signal on the isometric primer extension products.

2. (amended) The method according to claim 1, wherein the at least one primer is selected from the group consisting of a nucleic acid primer, an oligodeoxyribonucleotide, an oligoribonucleotide, and a copolymer of deoxyribonucleic acid and ribonucleic acid.

3. (amended) The method according to claim 1, wherein the target nucleic acid is selected from the group consisting of a deoxyribonucleic acid, a ribonucleic acid, and a copolymer of deoxyribonucleic acid and ribonucleic acid.

4. (amended) The method according to claim 1, wherein the non-terminator nucleotides are selected from the group consisting of deoxyribonucleotides and ribonucleotides.

6. (amended) The method according to claim 1, wherein the non-terminator nucleotide mixture comprises:

(a) dATP, dCTP, dGTP;

(b) dATP, dCTP, dTTP or dUTP;

(c) dATP, dGTP, dTTP or dUTP; or

(d) dCTP, dGTP, dTTP or dUTP.

9. (amended) The method according to claim 1, wherein said detectable marker is selected from the group consisting of an enzyme moiety, protein moiety, radioactive isotope, fluorescent moiety, and a chemical group.

11. (amended) The method according to claim 1, wherein the primer extension products are formed using a template-dependent enzyme.

12. (amended) The method according to claim 11, wherein the template-dependant enzyme is selected from the group consisting of DNA polymerase, RNA polymerase, and reverse transcriptase.

13. (amended) The method according to claim 11, wherein the template-dependant enzyme is *E. coli* DNA polymerase I, a Klenow fragment thereof, T4 DNA polymerase, T7 DNA polymerase, Thermophilic DNA polymerase, retroviral reverse transcriptase, or a combination thereof.

14. (amended) The method according to claim 1, wherein the target nucleic acid is synthesized enzymatically *in vivo*, or *in vitro*.

18. (amended) The method according to claim 1, wherein the target nucleic acid is selected from the group consisting of genomic DNA from an organism, RNA transcripts thereof, and cDNA prepared from RNA transcripts thereof.

19. (amended) The method according to claim 18, wherein the organism is a plant, microorganism, bacteria, or virus.

22. (amended) The method according to claim 21, wherein the mammal is a human being.

24. (amended) The method according to claim 23, wherein the amplification step comprises an amplification method selected from the group consisting of cloning, transcription, polymerase chain reaction (PCR), ligase chain reaction (LCR), strand displacement amplification (SDA), and loop mediated isothermal amplification (LAMP).

25. (amended) The method according to claim 1, wherein the primer comprises at least one moiety that permits affinity separation of the primer from the unincorporated reagent or the nucleic acid of interest.

26. (amended) The method according to claim 1, wherein the primer comprises at least one moiety that allows immobilization of the primer onto a solid support to produce an immobilized primer sequence.

27. (amended) The method according to claim 25 or 26, wherein the at least one moiety comprises a special chemical group selected from the group consisting of biotin, and digitonin.

28. (amended) The method according to claim 25 or 26, wherein the at least one moiety comprises a nucleotide sequence that allows the primer to link to a solid support, the solid support having a complementary sequence to the nucleotide sequence of the at least one moiety, wherein the primer links to the solid support via base pairing to the complementary sequence present in the solid support.

31. (amended) The method according to claim 1, wherein the primer is immobilized onto a solid support to produce immobilized isometric primer extension products.

32. (amended) The method according to claim 1, wherein the primer is reversibly immobilized onto a solid support.

33. (amended) The method according to claim 32, wherein the primer is cleaved from the solid support by a chemical, enzymatic or physical process.

34. (amended) The method according to claim 1, wherein the target nucleic acid is immobilized onto a solid support to produce immobilized isometric primer extension products.

36. (amended) The method according to claim 34, wherein the target nucleic acid is cleaved from the solid support by a chemical, enzymatic or physical process.

37. (amended) The method according to claim 31, 32, 34 or 35, wherein immobilization is accomplished via a photocleavable bond.

38. (amended) The method according to claim 26, 29, 31, 32, 34 or 35, wherein the solid support is selected from the group consisting of beads, flat surfaces, chips, capillaries, pins, and wafers.

Please add the following new claims.

41. (new) A method to detect or quantify at least one nucleic acid in a sample, the method comprising the steps of:

(a) annealing a primer to a target nucleic acid;

(b) extending the primer to form isometric primer extension products incorporating at least one fluorescently labeled nucleotide by omitting at least one of four required types of nucleotides for continuous extension during primer extension reactions; and

(c) assaying for incorporation of the fluorescently labeled nucleotide within the isometric extension products.

42. (amended) A method for detecting or quantifying a target nucleic acid in a sample comprising:

(a) preparing at least one primer specifically matched to a predetermined position of the target nucleic acid;

(b) annealing the at least one primer from (a) with the target nucleic acid to obtain a primer-nucleic acid duplex at the predetermined position of the target nucleic acid;

(c) mixing the primer-nucleic acid duplex from (b) with a non-terminator nucleotide mixture, wherein at least one of four required types of nucleotides for continuous extension during primer extension reactions is omitted from the non-terminator nucleotide mixture;

(d) performing isometric primer extension by enzymatic or chemical reaction wherein the primer extension terminates at a target nucleic acid nucleotide complementary to the omitted non-terminator nucleotide of (c); and

(e) detecting or quantifying the amount of isometric primer extension products.

43. (new) A method for detecting or quantifying a target nucleic acid in a sample comprising:

(a) annealing at least one primer to a target nucleic acid, wherein the primer is labeled with a detectable marker;

(b) extending the labeled primer to form isometric primer extension products by omitting at least one of four required types of nucleotides for continuous extension during primer extension reactions; and

(c) detecting the labeled primer extension product.

44. (new) The method of claim 42, wherein the amount of labeled primer extension products are detected or quantified by size selection separation and UV absorbance, dye stain, or mass spectrometry.

45. (new) The method according to claim 1, wherein the target nucleic acid is synthesized non-enzymatically.

46. (new) The method according to claim 28, wherein the solid support is selected from the group consisting of beads, flat surfaces, chips, capillaries, pins, and wafers.

47. (new) The method according to claim 1, wherein the non-terminator nucleotides are selected from the group consisting of modified deoxyribonucleotides and modified ribonucleotides.